

STN SEQUENCE

SEARCH FOR

510-567

NEW REGISTRY = 600 BAY 11

Trying 3106016892...Open

Welcome to STN International! Enter x:x
LOGINID:sssptal633cxd
PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 Sep 29 The Philippines Inventory of Chemicals and Chemical
Substances (PICCS) has been added to CHEMLIST
NEWS 3 Oct 27 New Extraction Code PAX now available in Derwent
Files
NEWS 4 Oct 27 SET ABBREVIATIONS and SET PLURALS extended in
Derwent World Patents Index files
NEWS 5 Oct 27 Patent Assignee Code Dictionary now available
in Derwent Patent Files
NEWS 6 Oct 27 Plasdoc Key Serials Dictionary and Echoing added to
Derwent Subscriber Files WPIDS and WPIX
NEWS 7 Nov 29 Derwent announces further increase in updates for DWPI
NEWS 8 Dec 5 French Multi-Disciplinary Database PASCAL Now on STN
NEWS 9 Dec 5 Trademarks on STN - New DEMAS and EUMAS Files
NEWS 10 Dec 15 2001 STN Pricing
NEWS 11 Dec 17 Merged CEABA-VTB for chemical engineering and
biotechnology
NEWS 12 Dec 17 Corrosion Abstracts on STN
NEWS 13 Dec 17 SYNTHLINE from Prous Science now available on STN
NEWS 14 Dec 17 The CA Lexicon available in the CAPLUS and CA files
NEWS 15 Jan 05 AIDSLINE is being removed from STN
NEWS 16 Feb 06 Engineering Information Encompass files have new names
NEWS 17 Feb 16 TOXLINE no longer being updated

NEWS EXPRESS FREE UPGRADE 5.0e FOR STN EXPRESS 5.0 WITH DISCOVER!
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NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
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Enter NEWS followed by the item number or name to see news on that
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 16:57:37 ON 07 MAR 2001

=> file registry

COST IN U.S. DOLLARS

FULL ESTIMATED COST

SINCE FILE	TOTAL
ENTRY	SESSION
0.15	0.15

FILE 'REGISTRY' ENTERED AT 16:58:05 ON 07 MAR 2001
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STRUCTURE FILE UPDATES: 6 MAR 2001 HIGHEST RN 325952-54-3
DICTIONARY FILE UPDATES: 6 MAR 2001 HIGHEST RN 325952-54-3

TSCA INFORMATION NOW CURRENT THROUGH July 8, 2000

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Structure search limits have been increased. See HELP SLIMIT
for details.

=> s CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQEN

0 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQEN
5055 SQL=58

L1 0 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQEN

(CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQ
EN AND SQL=58)

=> FILE DGENE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	10.96	11.11

FILE 'DGENE' ENTERED AT 17:07:39 ON 07 MAR 2001
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FILE LAST UPDATED: 05 MAR 2001 <20010305/UP>
LATEST DERWENT WEEK COMPREHENSIVELY COVERED: 200061

>>> PRICE INCREASES !!!! - SEE HELP COST <<<

>>> HOMOLOGY SEARCH FOR NUCLEOTIDES NOW AVAILABLE -
NEW GETSIM SEARCH FIELD CODES /SQP, /SQN, /TSQN
MUST BE SPECIFIED - SEE NEWS <<<

>>> HOMOLOGY BATCH SEARCH NOW AVAILABLE - SEE HELP SBATCH <<<

=> s CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQEN

SEARCH NOT VALID, USE RUN GETSEQ

=> RUN GETSEQ CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT

TYPE OF SEARCH ? (SQSP):HELP

For searching sequences with the GETSEQ run package, different
options are available. Each requires the corresponding field
qualifier:

Nucleic acid sequence:

SQEN: Exact Sequence Search of Nucleic Acids

SQSN: Subsequence Search of Nucleic Acids (exact sequences and
sequences with embeded query sequence)

Protein sequence:

SQEF: Exact Sequence Search of Proteins
 SQEFP: Exact Family Sequence Search of Proteins (answers that exactly match the query and answers in which family-equivalent substitution of the query amino acids occurs.)
 SQSP: Subsequence Search of Proteins (exact answers plus sequences in which query sequence is embedded.)
 SQSFP: Subsequence Family Search of Proteins (exact sequences, subsequences, and answers in which family-equivalent substitution of the query amino acids occurs)

TYPE OF SEARCH ? (SQSP):SQEN

L2 RUN STATEMENT CREATED

L2 0 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCG
 GTCTTGCT/SQEN

=> NEWS

NEWS 17	Feb 16	TOXLINE no longer being updated
NEWS 16	Feb 6	Engineering Information Encompass files have new names
NEWS 15	Jan 5	AIDSLINE is being removed from STN
NEWS 14	Dec 17	The CA Lexicon available in the CAPLUS and CA files
NEWS 13	Dec 17	SYNTHLINE from Proust Science now available on STN
NEWS 12	Dec 17	Corrosion Abstracts on STN
NEWS 11	Dec 17	Merged CEABA-VTB for chemical engineering and biotechnology
NEWS 10	Dec 15	2001 STN Pricing
NEWS 9	Dec 5	Trademarks on STN - New DEMAS and EUMAS Files
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NEWS 7	Nov 29	Derwent announces further increase in updates for DWPI
NEWS 6	Oct 27	Plasdoc Key Serials Dictionary and Echoing added to Derwent Subscriber Files WPIDS and WPIX
News 5	Oct 27	Patent Assignee Code Dictionary now available in Derwent Patent Files
NEWS 4	Oct 27	SET ABBREVIATIONS and SET PLURALS extended in Derwent World Patents Index files
NEWS 3	Oct 27	New Extraction Code PAX now available in Derwent Files
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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America

NEWS EXPRESS	FREE UPGRADE 5.0e FOR STN EXPRESS 5.0 WITH DISCOVER! (WINDOWS) NOW AVAILABLE
NEWS HOURS	STN Operating Hours
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and NEWS Items
NEWS PHONE	Direct Dial and Telecommunication Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

To see recent updates for a specific file, you must be in the file and enter "NEWS FILE". To see a list of all files available on STN, enter "HELP FILE NAMES". For a list of currently unavailable files enter "HELP FILES UNAVAILABLE".

=> HELP GETSIM

The GETSEQ run package is a tool to search the DGENE database for the protein and nucleic acid sequence data. The query used with GETSEQ may be prepared with the QUERY command, or may be entered directly within the GETSEQ run package. Below, the different approaches to use RUN GETSEQ are shown. Also, the query L-number may derive from a previous sequence search in another STN file with biosequence search capabilities, e.g. the REGISTRY file.

Maximum length of sequence queries are listed up in HELP QLIMITS.

=> QUE YADAIF/SQSP

L1 QUE YADAIF/SQSP

=> RUN GETSEQ L1

L2 RUN STATEMENT CREATED

L2 187 YADAIF/SQSP

=> RUN GETSEQ

PLEASE ENTER SEQUENCE QUERY : YADAIF

TYPE OF SEQUENCE ? (N OR P): P

L3 RUN STATEMENT CREATED

L3 187 YADAIF/SQSP

=> RUN GETSEQ

PLEASE ENTER SEQUENCE QUERY : YADAIF/SQSP

L4 RUN STATEMENT CREATED

L4 187 YADAIF/SQSP

=> RUN GETSEQ YADAIF/SQSP

L5 RUN STATEMENT CREATED

L5 187 YADAIF/SQSP

=> D HIT

L5 ANSWER 1 OF 187 DGENE COPYRIGHT 1995 DERWENT INFORMATION LTD
SEQ

1 yadaiftnsy rkvlqqlsar kllqdimrsq qgesnqerga rarlg
=====

HITS AT: 1-6

The following help messages contain details about biosequence searching in DGENE:

HELP AAC-
HELP NUC
HELP QLIMITS
HELP SEQUENCE
HELP SIM
HELP SQQ
HELP SSQ

The HELP RUN message describes the use of the RUN command in general.

=> HELP NUC

The following table lists the symbols and ambiguity codes for

nucleotides according to the IUPAC system that may be used in nucleic acid sequence searches employing RUN GETSEQ.

Codes	Name or Definition
-----	-----
A	Adenine
G	Guanine
U	Uracil
R	A or G
S	C or G
K	G or T/U
H	A, C or T/U; not G
B	C, G or T/U; not A
C	Cytosine
T	Thymine
M	A or C
W	A or T/U
Y	C or T/U
V	A, C or G; not T/U
D	A, G or T/U; not C
N	Unknown or Other

Modified bases are represented by the parent base or by N with the annotations added in the feature table. There are standard abbreviations for the most common modified bases available.

Exact Sequence Searches of Nucleic Acids (/SQEN) allow all codes and match the codes in the query exactly against the codes in the database.

Subsequence searches allow the requested sequences to be a subsequence of the sequences in the database.

Broad queries can also be composed employing the methods exemplified in HELP SQQ.

=> HELP SEQUENCE

Protein and nucleic acid sequence data are searchable and displayable in the DGENE File. Search of sequence data is either carried out with the GETSEQ RUN package or with the GETSIM RUN package. For information on how to use the RUN command, please consult the HELP RUN message. For information on using amino acid or nucleic acid codes to retrieve biosequences in the DGENE File, please consult the following help messages:

HELP AAC	- table of the 1- and 3-letter codes for common amino acids
HELP EFIELDS	- list of codes that may be used in SELECT
HELP GETSEQ	- biosequence searching with GETSEQ
HELP NUC	- codes for nucleic acids
HELP QLIMITS	- limits of sequence queries
HELP SIM	- similarity (homology) search for protein and nucleotide sequence data with GETSIM
HELP SQQ	- variability symbols in subsequence queries
HELP SSQ	- biosequence search methods and fields

For information on displaying sequences in the DGENE File, please consult the following help messages:

HELP DFIELDS	- list of display field codes
HELP FORMAT	- list of pre-defined formats

HELP HIGHLIGHTING - highlighting information

For information on the costs for searching and displaying biosequences, enter HELP COST at an arrow prompt (=>).

=> HELP SSQ

Sequence information may be retrieved from the DGENE File using a variety of search fields within the GETSEQ run package or using the GETSIM run package for similarity search of protein sequences. Queries may be prepared with the QUERY command and the search then carried out within the GETSEQ or GETSIM run package using the L-Number resulting from the QUERY generation, or the query may be directly created and carried out in one step within these run packages. The package is started with the command RUN GETSEQ or RUN GETSIM, respectively, at an arrow prompt (see also HELP RUN and HELP GETSEQ and HELP SIM).

Protein Sequences

GETSEQ

Four options are available in the GETSEQ run package for searching protein sequences using amino acid codes. Each requires the corresponding field qualifier described below. The sequence query is input using 1- and/or 3-letter codes for the amino acids. Enter HELP AAC at an arrow prompt (=>) in the DGENE File for a list of codes for the common amino acids. Enter HELP SQQ at an arrow prompt for information on symbols used to allow for variability in subsequence queries.

Exact Sequence Search of Proteins (/SQEP) retrieves sequences that exactly match the search query. The search query must be completely defined. Variability symbols are not allowed.

Exact Family Sequence Search of Proteins (/SQEFP) retrieves answers that exactly match the query and answers in which family-equivalent substitution of the query amino acids occurs. Variability symbols are not allowed.

Subsequence Search of Proteins (/SQSP) retrieves exact answers plus sequences in which the query sequence is embedded. Variability symbols are allowed.

Subsequence Family Search of Proteins (/SQSFP) retrieves exact sequences, subsequences, and answers in which family-equivalent substitution of the query amino acids occurs. For example, the query ADHIFC/SQSFP retrieves the equivalent fragment ...PQKLYC..

The families of amino acid equivalents retrieved in protein family searches are:

P, A, G, S, T	(neutral, weakly hydrophobic)
Q, N, E, D, B, Z	(hydrophilic, acid amine)
H, K, R	(hydrophilic, basic)
L, I, V, M	(hydrophobic)
F, Y, W	(hydrophobic, aromatic)
C	(cross-link forming)

In addition to these sequence search methods with the GETSEQ run package, you also have the option of searching the following fields with text or numeric information on protein sequence

Features:

Definition

Search Code

Amino Acid
Amino Acid Count
Sequence Length

/AA
/AA.CNT
/SQL

The /SQL field is a numeric field and may be searched with numeric operators or ranges, e.g. 100-200/SQL.

A GETSEQ protein sequence query (i.e. a query consisting of one or more of these fields: /SQEP, /SQSP, /SQEFP, /SQSFP) may be combined directly in a single search with only the following fields: /FS, /UP. However, any sequence L-numbered answer set from RUN GETSEQ may be combined with any search field in the DGENE File (e.g. => S L10 AND US/PC, where L10 represents the answer set from a RUN GETSEQ operation).

GETSIM

The GETSIM run package requires only the sequence query without any specification of the search. The minimum stem length of the amino acids sequence query must be 5. Variability symbols are not allowed, enter HELP AAC at an arrow prompt in the DGENE file for a list of allowed codes for the common amino acids.

In addition to these sequence search methods with the GETSEQ or GETSIM run package you also have the option of searching the following fields with information on nucleic acid sequence features:

Definition

Search Code

Nucleic Acid
Nucleic Acid Count
Sequence Length

/NA
/NA.CNT
/SQL

The /SQL field is a numeric field and may be searched with numeric operators or ranges, e.g. 100-200/SQL

Nucleic Acid Sequences

Two options are available in the GETSEQ run package for searching nucleic acid sequences using 1-letter codes. Each requires the corresponding field qualifier described below. Enter HELP NUC at an arrow prompt in the DGENE File for a list of codes for nucleic acids. Enter HELP SQQ for information on symbols used to allow for variability in subsequence queries.

Exact Sequence Search of Nucleic Acids (/SQEN) retrieves sequences that exactly match the search query. The search query must be completely defined. Ambiguity codes for nucleic acids are allowed. Variability symbols are not allowed.

Subsequence Search of Nucleic Acids (/SQSN) retrieves exact answers plus sequences in which the query sequence is embedded. Variability symbols are allowed.

A GETSEQ nucleic acid sequence query (i.e. a query consisting of one or more of these fields: /SQEN, /SQSN) may be combined directly in a single search with only the following fields: /FS, /UP. However, any sequence field may be combined with any

Search field in the DGENE file (e.g. => S L10 AND US/PC, where
L10 represents the answer set from a RUN GETSEQ operation).

=> RUN GETSEQ CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQSN

L3 RUN STATEMENT CREATED

L3 0 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCG
GTCTTGCT/SQSN

=> FILE REGISTRY

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

65.66

76.77

FILE 'REGISTRY' ENTERED AT 17:30:47 ON 07 MAR 2001

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STRUCTURE FILE UPDATES: 6 MAR 2001 HIGHEST RN 325952-54-3

DICTIONARY FILE UPDATES: 6 MAR 2001 HIGHEST RN 325952-54-3

TSCA INFORMATION NOW CURRENT THROUGH July 8, 2000

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Structure search limits have been increased. See HELP SLIMIT
for details.

=> S CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQSN

L4 1 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCCTCTTGGCCTCTCTCGGTCTTGCT/SQSN

=> D SEQ NTE LC 1

L4 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2001 ACS

SEQ 1 aattcctgga caacaatccc tttgagagt atagtaagg ggatgaactg
51 agatgctaag ctacgttct tcgcttggt gtaggtgcc ccatgtcttg
101 gtttagtgct tctctccacc ctatagctt agccattgct tgtccaatcc
151 cattcccatc tcgcatcacg ctctatttat gaccaaggct gtcaaagtga
201 agccccactc atgtggcctc cacttcatat tgttttcttt gtcgataaga
251 ctgtcatccc gtctccggtg gcttcacga agaacgattt gtaaagatgg
301 atagcgatag gctgcccttg gtcggtatga agccgaagtc cctcgtgcct
351 cgatggatat gcgcttcaac ccgacgcaca gcgcacgtgg tatccgaatg
401 ggacggaaaag gtagctcctc cagtgggcta tataagcctt tccctggccg
451 ggctcagact ccctagcaag cagcattggt caagctcacg acctcaatcc
501 gcgagtaaac atgaagtcca ccgctctgct tactggcttc ggctcttg
= =====
551 cctctctcgg tcttgctagc cctgtcacgt ccgagtatac gagcgtgcga
=====

601 gaagcccctt tcggatacaa gcctggctcc aaggagtcca ttgagaactt
651 gaaggacaag gtcgagaaca ttgtctggct tattctcgag aacagggttg
701 tgtgccctta cgatattcat atgtggaata ataaattcct caattcagct
751 tgtggtatgt gaagacgagc actaacatat ggtccagatc cttcgataac
801 attctgggag gcgtgcgccg ccaaggactg gacaaccgga tcaacaacgg
851 cccgttctgc aactacaaga atgcgagcga cccatcctcg ggcaagtact
901 gtactcaggc caaggactat gattccgtgt tcaacgatcc agaccactcc
951 gtgactggta ataacttga gttctacgga acttacaccc caaacaatgg
1001 tgcgattgcc agtggaagg tcgtcgccga ccagtctggc ttcctcaacg
1051 cacagcttaa cgactacccc aaactggccc cagaagaggc gacaaggcaa
1101 gtgatgggat actatacgga ggaggaggt cctacgctcg tggaccttgt


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1151 ggatgagttc actactttca acagctgggtt ctcgtgtgtt cctggcgtaa
1201 gtgcgataaa tctgtatatt tttaattttg actaacgctg tcaaaagcct
1251 accaacccca accgcttggt cgctctggca ggaaccgctg ctgggcatgg
1301 caagaatgac gatgacttcc tgaactatgg tatctctagc aagtccatct
1351 tcgaggccgc caacgagaag ggcgtgtcct ggctcaacta cgatggcacc
1401 aacggagaat tcgaaccgga ttctctcttc ttcacctacg tcaaccagac
1451 ctcccgggtcc aacgtgggtgc ccgttgaaaa cttcttccaa gacgcctacc
1501 tcggtgtcct ccctaaattc tcttacatta acccctcctg ctgcggcacc
1551 aacaccaact ccatgcaccc caccggtaac gtctcctacg gtgaggtctt
1601 cgtcaagcag atctatgatg ccattcgcca gggccctcag tgggacaaga
1651 ccctgctctt cattacctac gacgagaccg gtggcttcta cgaccatgtc
1701 cctccccctc tcgccgtccg cccggacaac ctgacctaca ctgagactgc
1751 gaagaacggt cagaaatata ctcttcactt cgaccgtctg ggtggccgca
1801 tgccgacctg gggttatctc cttacagta agaagggata catcgagcag
1851 tacggaacgg atcccgtcac gggcaagccc gctccctaca gtgctacctc
1901 cgtcctcaag actctcggat atctctggga catcgaggac ttcaccctc
1951 gtgtcgccca ctctccatct ttcgatcacc tgatcggcac gactttgcgt
2001 gaggatgctc ctattgctct caagactccc catacctttt cgggtataagt
2051 ctcagtccgt gcagtgcagc aggattaaaa gtgatgatga acgttctgac
2101 ttcagtgaac gattacatgt tatagagcat tgttttgctt atagctacgc
2151 ctagagcgag cgcgatgatg ataagataaa gctgggttat ttctctattg
2201 tatattcatt aatgaaagac ttgataaca tgggatttaa aaaggaaatg
2251 ttttcttgca caatcaactc acggaacagg cgtaacttta cgatgactgc
2301 accccggata cattaatt

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HITS AT: 510-567

NTE doublestranded

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

=> FILE CAPLUS

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
32.31	109.08

FULL ESTIMATED COST

FILE 'CAPLUS' ENTERED AT 17:34:21 ON 07 MAR 2001
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FILE COVERS 1967 - 7 Mar 2001 VOL 134 ISS 11
 FILE LAST UPDATED: 6 Mar 2001 (20010306/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

Now you can extend your author, patent assignee, patent information, and title searches back to 1907. The records from 1907-1966 now have this searchable data in CAOLD. You now have electronic access to all of CA: 1907 to 1966 in CAOLD and 1967 to the present in CAPLUS on STN.

The CA Lexicon is now available in the Controlled Term (/CT) field. Enter HELP LEXICON for full details.

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=> S L4

L5 1 L4

=> D IBIB ABS L5

L5 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:802341 CAPLUS
DOCUMENT NUMBER: 133:345609
TITLE: Phospholipase B and its gene from *Aspergillus oryzae*
for use in improving stability and decreasing
stickiness of dough in baking
INVENTOR(S): Harris, Paul; Brown, Kimberly M.
PATENT ASSIGNEE(S): Novo Nordisk Biotech, Inc., USA
SOURCE: U.S., 24 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6146869	A	20001114	US 1999-426072	19991021

AB The present invention relates to isolated polypeptides having phospholipase B activity and isolated nucleic acid sequences encoding the polypeptides from *Aspergillus oryzae* HowB430. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the nucleic acid sequences as well as methods for producing and using the polypeptides. Thermostability and other properties of this phospholipase B suggest it may be useful in increasing stability and decreasing stickiness of dough in the prepn. of bakery products.

REFERENCE COUNT: 5

REFERENCE(S):

CAPLUS

- (1) Leidich; J Biol Chem 1998, V273(40), P26078
- (2) Masuda; Eur J Biochem 1991, V202, P783 CAPLUS
- (3) Masuda; Eur J Biochem 1998, V202, P783
- (4) Memon; FEMS Microbiology Letters 1983, V18, P15 CAPLUS
- (5) Sugiyama; Nedical Mycology 1998, V37, P61